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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2010; month=11; day=19; hr=16; min=38; sec=55; ms=869;  
]

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Application No: 10594262 Version No: 3.0

**Input Set:**

**Output Set:**

**Started:** 2010-11-15 15:46:57.159  
**Finished:** 2010-11-15 15:47:00.137  
**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 978 ms  
**Total Warnings:** 31  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 33  
**Actual SeqID Count:** 33

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W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
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**Input Set:**

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**Started:** 2010-11-15 15:46:57.159  
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Error code	Error Description
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<130> H1776 US  
<140> 10594262  
<141> 2010-11-15

<150> EP 04 00 7278.7  
<151> 2004-03-26

<150> US 60/570,497  
<151> 2004-05-13

<160> 33

<170> PatentIn version 3.3

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<223> /note="Description of artificial sequence: polypeptides with affinity to the Tet repressor"

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<223> /note="Description of artificial sequence: polypeptides with affinity to the Tet repressor"

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<220>  
<223> /note="Description of artificial sequence: polypeptides with affinity to the Tet repressor"

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Ser Gly Gly Ala Trp Thr Trp Asn Ala Tyr Ala Phe Ala Ala Pro Ser  
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Gly Gly Gly Ser  
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<223> /note="Description of artificial sequence: polypeptides with affinity to the Tet repressor"

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1 5 10 15

Gly Gly Gly Ser  
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<212> PRT  
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<223> /note="Description of artificial sequence: polypeptides with  
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Ser Gly Gly Ala Trp Thr Trp Asn Ala Tyr Ala Phe Ala Ala Pro Ala  
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Gly Gly Gly Ser  
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Gly Arg Gly Ser  
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<223> /note="Description of artificial sequence: polypeptides with  
affinity to the Tet repressor"

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Ser Gly Gly Ala Trp Thr Trp Asn Ala Tyr Ala Phe Ala Ala Pro Ser  
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Asp Gly Gly Leu  
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<223> /note="Description of artificial sequence: polypeptides with  
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Ser Gly Gly Ala Trp Thr Trp Asn Ala Tyr Ala Phe Ala Ala Pro Ser  
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Gly Glu Gly Ser  
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Ser Gly Gly Ala Trp Thr Trp Asn Ala Tyr Ala Phe Ala Ala Pro Ser  
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Gly Gly Gly Trp  
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Ser Gly Gly Ala Trp Thr Trp Asn Ala Tyr Ala Phe Ala Ala Pro Ser  
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Gly Gly Cys Ser  
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Gly Gly Asp Ser  
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<223> /note="Description of artificial sequence: polypeptides with  
affinity to the Tet repressor"

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Ser Gly Gly Ala Trp Thr Trp Asn Ala Tyr Ala Phe Ala Ala Pro Ser  
1 5 10 15

Gly Gly Arg Ser  
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<210> 14  
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<212> PRT  
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<223> /note="Description of artificial sequence: polypeptides with  
affinity to the Tet repressor"

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Ser Gly Gly Ala Trp Thr Trp Asn Ala Phe Ala Phe Ala Ala Pro Ser  
1 5 10 15

Gly Gly Gly Ser  
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<210> 15  
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<212> PRT  
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<220>  
<223> /note="Description of artificial sequence: polypeptides with  
affinity to the Tet repressor"

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Asn Ala Tyr Ala Phe Ala Ala Pro Ser Gly Gly Ser  
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<210> 16  
<211> 30  
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<220>  
<223> /note="Description of artificial sequence: polypeptides with  
affinity to the Tet repressor"

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Trp Asn Ala Tyr Ala Phe Ala Ala Pro Ser Gly Gly Ser  
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Trp Asn Ala Tyr Ala Phe Ala Ala Pro Ser Gly Gly Ser  
20 25 30

<210> 18  
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<400> 18

Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu  
1 5 10 15

Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln  
20 25 30

Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys  
35 40 45

Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His  
50 55 60

Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg  
65 70 75 80

Asn Asn Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly  
85 90 95

Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr  
100 105 110

Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu  
115 120 125

Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys  
130 135 140

Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr  
145 150 155 160

Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu  
165 170 175

Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu  
180 185 190

Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser  
195 200 205

<210> 19

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<212> PRT  
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<223> /note="Description of artificial sequence: tTA (TetR-VP16)"

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Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln  
20 25 30

Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys  
35 40 45

Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His  
50 55 60

Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg  
65 70 75 80

Asn Asn Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly  
85 90 95

Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr  
100 105 110

Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu  
115 120 125

Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys  
130 135 140

Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr  
145 150 155 160

Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu  
165 170 175

Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu  
180 185 190

Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala

195

200

205

Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly  
210 215 220

Leu Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala  
225 230 235 240

Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser  
245 250 255

Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp  
260 265 270

Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp  
275 280 285

Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro  
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His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe  
305 310 315 320

Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly  
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<223> /note="Description of artificial sequence: tTA2 (TetR-FFF)"

<400> 20

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1 5 10 15

Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln  
20 25 30

Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys  
35 40 45

Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His  
50 55 60

Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg  
65 70 75 80

Asn Asn Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly  
85 90 95

Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr  
100 105 110

Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu  
115 120 125

Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys  
130 135 140

Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr  
145 150 155 160

Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu  
165 170 175

Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu  
180 185 190

Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Gly Pro  
195 200 205

Ala Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Pro Ala Asp Ala  
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Leu Asp Asp Phe Asp Leu Asp Met Leu Pro Ala Asp Ala Leu Asp Asp  
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Phe Asp Leu Asp Met Leu Pro Gly  
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<400> 21

Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu  
1 5 10 15

Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln  
20 25 30

Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys  
35 40 45

Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His  
50 55 60

Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg  
65 70 75 80

Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly  
85 90 95

Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr  
100 105 110

Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu  
115 120 125

Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys  
130 135 140

Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr  
145 150 155 160

Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu  
165 170 175

Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu  
180 185 190

Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ser  
195 200 205

Glu Phe Gln Tyr Leu Pro Asp Thr Asp Asp Arg His Arg Ile Glu Glu  
210 215 220

Lys Arg Lys Arg Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys Lys Ser  
225 230 235 240

Pro Phe Ser Gly Pro Thr Asp Pro Arg Pro Pro Pro Arg Arg Ile Ala  
245 250 255

Val Pro Ser Arg Ser Ser Ala Ser Val Pro Lys Pro Ala Pro Gln Pro  
260 265 270

Tyr Pro Phe Thr Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu Phe Pro  
275 280 285

Thr Met Val Phe Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala Leu Ala  
290 295 300

Pro Ala Pro Pro Gln Val Leu Pro Gln Ala Pro Ala Pro Ala Pro Ala  
305 310 315 320

Pro Ala Met Val Ser Ala Leu Ala Gln Ala Pro Ala Pro Val Pro Val  
325 330 335

Leu Ala Pro Gly Pro Pro Gln Ala Val Ala Pro Pro Ala Pro Lys Pro  
340 345 350

Thr Gln Ala Gly Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln Leu Gln  
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Phe Asp Asp Glu Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr Asp Pro  
370 375 380

Ala Val Phe Thr Asp Leu Ala Ser Val Asp Asn Ser Glu Phe Gln Gln  
385 390 395 400

Leu Leu Asn Gln Gly Ile Pro Val Ala Pro His Thr Thr Glu Pro Met  
405 410 415

Leu Met Glu Tyr Pro Glu Ala Ile Thr Arg Leu Val Thr Gly Ala Gln  
420 425 430

Arg Pro Pro Asp Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly Leu Pro

435

440